Poster

The molecular architecture of *Lactobacillus* S-Layer: Assembly interactions

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S-layers are crystalline arrays found on bacterial and archaeal cells (Fig. 1). *Lactobacillus* is a diverse family of bacteria known especially for potential gut health benefits. This study focuses on the S-layer proteins from *Lactobacillus acidophilus* and *Lactobacillus amylovorus* common in the mammalian gut. Atomic resolution structures of *Lactobacillus* S-layer proteins SlpA and SlpX exhibit domain swapping and the obtained assembly model of the main S-layer protein SlpA aligns well with prior electron microscopy and mutagenesis data. The S-layer's pore size suggests a protective role, with charged areas aiding adhesion. A highly similar domain organization and interaction network are observed across the *Lactobacillus* genus. The structure of the SlpA S-layer and the suggested incorporation of SlpX, as well as its interaction with teichoic acids lays the foundation for deciphering its role in immune responses and for developing effective treatments for a variety of infectious and bacteria-mediated inflammation processes, opening new opportunities for targeted engineering of the S-layer or lactobacilli bacteria in general.

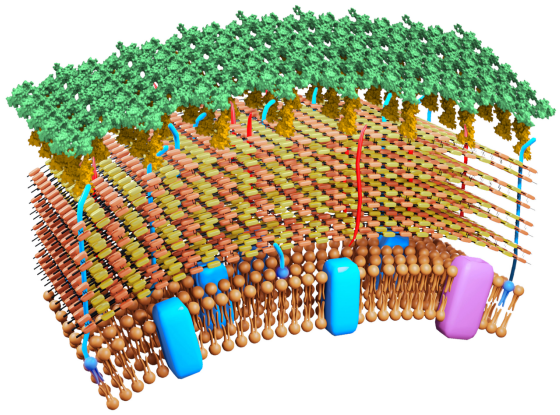

Figure 1. Schematic representation of the cell envelope of *Lactobacillus acidophilus* containing an S-layer.